



PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,451

DATE: 02/17/2002

TIME: 13:31:49

Input Set : A:\pto.txt

Output Set: N:\CRF3\02152002\I914451.raw

ENTERED

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3 <110> APPLICANT: Haeggstrm, Jesper Z
4      Pr, Nordlund
5      Thunissen, Marjolein
7 <120> TITLE OF INVENTION: Drug design based on the structure of LTA4 Hydrolase
9 <130> FILE REFERENCE: PVZ-006US
11 <140> CURRENT APPLICATION NUMBER: 09/914,451
12 <141> CURRENT FILING DATE: 2001-08-27
14 <150> PRIOR APPLICATION NUMBER: SE 9900722.1
15 <151> PRIOR FILING DATE: 1999-02-26
17 <150> PRIOR APPLICATION NUMBER: 60/122,110
18 <151> PRIOR FILING DATE: 1999-02-26
20 <160> NUMBER OF SEQ ID NOS: 1
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 610
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
30 Pro Glu Ile Val Asp Thr Cys Ser Leu Ala Ser Pro Ala Ser Val Cys
31   1           5           10           15
33 Arg Thr Lys His Leu His Leu Arg Cys Ser Val Asp Phe Thr Arg Arg
34           20           25           30
36 Thr Leu Thr Gly Thr Ala Ala Leu Thr Val Gln Ser Gln Glu Asp Asn
37           35           40           45
39 Leu Arg Ser Leu Val Leu Asp Thr Lys Asp Leu Thr Ile Glu Lys Val
40           50           55           60
42 Val Ile Asn Gly Gln Glu Val Lys Tyr Ala Leu Gly Glu Arg Gln Ser
43   65           70           75           80
45 Tyr Lys Gly Ser Pro Met Glu Ile Ser Leu Pro Ile Ala Leu Ser Lys
46           85           90           95
48 Asn Gln Glu Ile Val Ile Glu Ile Ser Phe Glu Thr Ser Pro Lys Ser
49           100          105          110
51 Ser Ala Leu Gln Trp Leu Thr Pro Glu Gln Thr Ser Gly Lys Glu His
52           115          120          125
54 Pro Tyr Leu Phe Ser Gln Cys Gln Ala Ile His Cys Arg Ala Ile Leu
55           130          135          140
57 Pro Cys Gln Asp Thr Pro Ser Val Lys Leu Thr Tyr Thr Ala Glu Val
58 145          150          155          160
60 Ser Val Pro Lys Glu Leu Val Ala Leu Met Ser Ala Ile Arg Asp Gly
61           165          170          175
63 Glu Thr Pro Asp Pro Glu Asp Pro Ser Arg Lys Ile Tyr Lys Phe Ile
64           180          185          190
66 Gln Lys Val Pro Ile Pro Cys Tyr Leu Ile Ala Leu Val Val Gly Ala

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67          195          200          205
69 Leu Glu Ser Arg Gln Ile Gly Pro Arg Thr Leu Val Trp Ser Glu Lys
70          210          215          220
72 Glu Gln Val Glu Lys Ser Ala Tyr Glu Phe Ser Glu Thr Glu Ser Met
73 225          230          235          240
75 Leu Lys Ile Ala Glu Asp Leu Gly Gly Pro Tyr Val Trp Gly Gln Tyr
76          245          250          255
78 Asp Leu Leu Val Leu Pro Pro Ser Phe Pro Tyr Gly Gly Met Glu Asn
79          260          265          270
81 Pro Cys Leu Thr Phe Val Thr Pro Thr Leu Leu Ala Gly Asp Lys Ser
82          275          280          285
84 Leu Ser Asn Val Ile Ala His Glu Ile Ser His Ser Trp Thr Gly Asn
85          290          295          300
87 Leu Val Thr Asn Lys Thr Trp Asp His Phe Trp Leu Asn Glu Gly His
88 305          310          315          320
90 Thr Val Tyr Leu Glu Arg His Ile Cys Gly Arg Leu Phe Gly Glu Lys
91          325          330          335
93 Phe Arg His Phe Asn Ala Leu Gly Gly Trp Gly Glu Leu Gln Asn Ser
94          340          345          350
96 Val Lys Thr Phe Gly Glu Thr His Pro Phe Thr Lys Leu Val Val Asp
97          355          360          365
99 Leu Thr Asp Ile Asp Pro Asp Val Ala Tyr Ser Ser Val Pro Tyr Glu
100          370          375          380
102 Lys Gly Phe Ala Leu Leu Phe Tyr Leu Glu Gln Leu Leu Gly Gly Pro
103 385          390          395          400
105 Glu Ile Phe Leu Gly Phe Leu Lys Ala Tyr Val Glu Lys Phe Ser Tyr
106          405          410          415
108 Lys Ser Ile Thr Thr Asp Asp Trp Lys Asp Phe Leu Tyr Ser Tyr Phe
109          420          425          430
111 Lys Asp Lys Val Asp Val Leu Asn Gln Val Asp Trp Asn Ala Trp Leu
112          435          440          445
114 Tyr Ser Pro Gly Leu Pro Pro Ile Lys Pro Asn Tyr Asp Met Thr Leu
115          450          455          460
117 Thr Asn Ala Cys Ile Ala Leu Ser Gln Arg Trp Ile Thr Ala Lys Glu
118 465          470          475          480
120 Asp Asp Leu Asn Ser Phe Asn Ala Thr Asp Leu Lys Asp Leu Ser Ser
121          485          490          495
123 His Gln Leu Asn Glu Phe Leu Ala Gln Thr Leu Gln Arg Ala Pro Leu
124          500          505          510
126 Pro Leu Gly His Ile Lys Arg Met Gln Glu Val Tyr Asn Phe Asn Ala
127          515          520          525
129 Ile Asn Asn Ser Glu Ile Arg Phe Arg Trp Leu Arg Leu Cys Ile Gln
130          530          535          540
132 Ser Lys Trp Glu Asp Ala Ile Pro Leu Ala Leu Lys Met Ala Thr Glu
133 545          550          555          560
135 Gln Gly Arg Met Lys Phe Thr Arg Pro Leu Phe Lys Asp Leu Ala Ala
136          565          570          575
138 Phe Asp Lys Ser His Asp Gln Ala Val Arg Thr Tyr Gln Glu His Lys
139          580          585          590

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141	Ala	Ser	Met	His	Pro	Val	Thr	Ala	Met	Leu	Val	Gly	Lys	Asp	Leu	Lys
142			595					600					605			
144	Val	Asp														
145			610													

## VERIFICATION SUMMARY

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